

SECRET

<120> Novel G Protein Coupled Receptors

<150> 60/184,305

<150> 60/188,880

<150> 60/219,492

<150> 60/173,339

<151> 1999-12-28

<150> 60/224,321

<151> 2000-08-11

<150> 60/200,534

<151> 2000-04-27

<150> 60/239,062

<151> 2000-10-09

<160> 56

<170> PatentIn version 3.0

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 gacattggag ctgagcagcc agaggactgc ccattcccc agcagcccac cgaggccgag 480
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<213> Homo sapiens

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<213> Homo sapiens

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Pro Trp Met Ala Leu Cys Val Leu Trp Cys Ser Val Ala Gln Ala Leu
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Leu Leu Pro Val Phe Leu Trp Ala Cys Asp Arg Tyr Arg Ala Asp Leu
35 40 45

Lys Ala Val Arg Glu Lys Cys Met Ala Leu Met Ala Asn Asp Glu Glu
50 55 60

Ser Asp Asp Gly Glu Asp Gly Leu Arg Val Ala Pro Gly Arg Val
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Leu Gly Asn Gly Ala Val Leu Trp Leu Leu Ser Ser Asn Val Tyr Arg
35 40 45

Asn Pro Phe Ala Ile Tyr Leu Leu Asp Val Ala Cys Ala Asp Leu Ile
50 55 60

Phe Leu Gly Cys His Met Val Ala Ile Val Pro Asp Leu Leu Gln Gly
65 70 75 80

Arg Leu Asp Phe Pro Gly Phe Val Gln Thr Ser Leu Ala Thr Leu Arg
85 90 95

Phe Phe Cys Tyr Ile Val Gly Leu Ser Leu Leu Ala Ala Val Ser Val
100 105 110

Glu Gln Cys Leu Ala Ala Leu Phe Pro Ala Trp Tyr Ser Cys Arg Arg
115 120 125

Pro Arg His Leu Thr Thr Cys Val Cys Ala Leu Thr Trp Ala Leu Cys
130 135 140

Leu Leu Leu His Leu Leu Leu Ser Gly Ala Cys Thr Gln Phe Phe Gly
145 150 155 160

Glu Pro Ser Arg His Leu Cys Arg Thr Leu Trp Leu Val Ala Ala Val
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Leu Leu Ala Leu Leu Cys Cys Thr Met Cys
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Leu	Val 35	Pro	Val	Thr	Ile	Pro	Arg 40	Val	Arg	Ala	Phe	His 45	Arg	Val	Pro
His 50	Asn	Leu	Val	Ala	Ser	Thr 55	Ala	Val	Ser	Asp	Glu 60	Leu	Val	Ala	Ala
Leu 65	Ala	Met	Pro	Pro	Ser 70	Leu	Ala	Ser	Glu	Leu 75	Ser	Thr	Gly	Arg	Arg 80
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<210> 18
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<213> Homo sapiens
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<400> 18

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Arg Asp Gly Ala Ile Thr Arg His Leu Gln His Thr Leu Arg Thr Arg
20 25 30

Ser Arg Ala Ser Leu Leu Met Ile Ala Leu Ala Arg Val Pro Ser Ala
35 40 45

Leu Ile Ala Leu Ala Pro Leu Leu Phe Gly Arg Gly Glu Val Cys Asp
50 55 60

Ala Arg Leu Gln Arg Cys Gln Val Ser Arg Glu Pro Ser Tyr Ala Ala
65 70 75 80

Phe Ser Thr Arg Gly Ala Phe His Leu Pro Leu Gly Val Val Pro Phe
85 90 95

Val Tyr Arg Lys Ile Tyr Glu Ala Ala Lys Phe Arg Phe Gly Arg Arg
100 105 110

Arg Arg Ala Val Leu Pro Leu Pro Ala Thr Met Gln Val Arg Gly Gly
115 120 125

Leu Arg Asn Val Ala Met Gly Lys Arg Leu Leu Glu Lys Glu Ala Ala
130 135 140

Ser Arg Met Gly Glu Trp Ala Glu Ala Cys Thr Asn Gly Ala Arg Ala
145 150 155 160

Gln Arg Ser Pro Gly Ala His Glu Asp Lys Phe Ala Ile Ser Ser Ser
165 170 175

Glu Ala Gly Thr Glu Gly Leu Val Thr Gly Ser Pro Gly Thr Gln Val
180 185 190

Arg Gly Ser Pro Ala Ala Tyr Leu Val Arg Ala Glu Glu Arg Val Ser
195 200 205

Gln Ser Ala Arg
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<210> 19

<211> 217

<212> PRT

<213> Homo sapiens

<400> 19

Met Asp Asp Asn Ala Thr Asn Thr Ser Thr Ser Phe Leu Ser Val Leu
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Asn Pro His Gly Ala His Ala Thr Ser Phe Pro Phe Asn Phe Ser Tyr
20 25 30

Ser Asp Tyr Asp Met Pro Leu Asp Glu Asp Glu Asp Val Thr Asn Ser
35 40 45

Arg Thr Phe Phe Ala Ala Lys Ile Val Ile Gly Met Ala Leu Gly
 50 55 60
 Ile Met Leu Val Cys Gly Ile Gly Asn Phe Ile Phe Ile Ala Ala Leu
 65 70 75 80
 Val Arg Tyr Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn
 85 90 95
 Leu Ala Ile Ser Asp Phe Leu Val Ala Ile Val Cys Cys Pro Phe Glu
 100 105 110
 Met Asp Tyr Tyr Val Val Arg Gln Leu Ser Trp Glu His Gly His Val
 115 120 125
 Leu Cys Thr Ser Val Asn Tyr Leu Arg Thr Val Ser Leu Tyr Val Ser
 130 135 140
 Thr Asn Ala Leu Leu Ala Ile Ala Ile Asp Arg Val Gln Gln Gln Trp
 145 150 155 160
 Gly Gln Gln Arg Arg Ser Gly Arg Lys Gly His Trp Asn Cys Pro Leu
 165 170 175
 Leu Tyr Cys Ser Cys Arg Leu Met Arg Gly Val Ser Ile Pro Pro Arg
 180 185 190
 Cys Gly Cys Met Gly Asp Ser Lys Ala Cys Pro Leu Thr Asp Ser Glu
 195 200 205
 Lys Ser Ser Pro Phe Pro Ala Leu Phe
 210 215

<210> 20
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 20 25 30
 Ile Ile Gln Asn Leu Pro Ala Leu Asn Ser Ala Ile Asn Pro Leu Ile
 35 40 45
 Tyr Cys Val Phe Ser Ser Ser Ile Ser Phe Pro Cys
 50 55 60

<210> 21
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<400> 21

Glu Lys Gln Ala Arg Val Leu Ile Val Ile Ala Trp Ser Leu Ser Phe
 1 5 10 15

Leu Phe Ser Ile Pro Thr Leu Ile Ile Phe Gly Lys Arg Thr Leu Ser
 20 25 30
 Asn Gly Glu Val Gln Cys Trp Ala Leu Trp Pro Asp Asp Ser Tyr Trp
 35 40 45
 Thr Pro Tyr Met Thr Ile Val Ala Phe Leu Val Tyr Phe Ile Pro Leu
 50 55 60
 Thr Ile Ile
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 <213> Homo sapiens
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 Ile Ser Tyr Ala Arg Asn Lys Ala Leu Pro His Trp Leu Cys His Asp
 20 25 30
 Tyr Asp Ile Leu Gly Val Trp Gly Ala Trp Val Val Arg Ile Pro Tyr
 35 40 45
 Arg Ser Pro Glu Ala Trp Gly Gly Pro Val Gly Asp Ala Arg Ser Leu
 50 55 60
 Cys Ser Thr Leu Pro His Ala Arg Leu Ser Asn Ala Lys Lys Gln Ala
 65 70 75 80
 Val His Thr Val Met Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala
 85 90 95
 Leu Pro Ala Val Gly Trp His Asp Thr Ser Glu Arg Phe Tyr Thr His
 100 105 110
 Gly Cys Arg Phe Ile Val Ala Glu Ile Gly Leu Gly Phe Gly Val Cys
 115 120 125
 Phe Leu Leu Leu Val Gly Gly Ser Val Ala Met Gly Val Ile Cys Thr
 130 135 140
 Ala Ile Ala Leu Phe Gln Thr Leu Ala Val Gln Val Gly Arg Gln Ala
 145 150 155 160
 Asp Arg Arg Ala Phe Thr Val Pro Thr Ile Val Val Glu Asp Ala Gln
 165 170 175
 Gly Lys Arg Arg Ser Ser Ile Asp Gly Ser Glu Pro Ala Lys Thr Ser
 180 185 190
 Leu Gln Thr Thr Gly Leu Val Thr Thr Ile Val Phe Ile Tyr Asp Cys
 195 200 205
 Leu Met Gly Phe Pro Val Leu Val
 210 215

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<210> 23
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<400> 23

Met Ser Asp Glu Arg Arg Leu Pro Gly Ser Ala Val Gly Trp Leu Val
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Cys Gly Gly Leu Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val
 20 25 30

Gly Ala Lys Gln Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr
 35 40 45

Leu Ala Ala Thr His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr
 50 55 60

Ser Val Val Gln Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu
 65 70 75 80

Gly Leu Cys Lys Val Phe Val Ser Thr Phe Tyr Thr Leu Thr Leu Ala
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Thr Cys Phe Ser Val Thr Ser Leu Ser Tyr His Arg Met Trp Met Val
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Cys Trp Pro Val Asn Tyr Arg
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<210> 24
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<400> 24

Met Asp Pro Thr Thr Pro Ala Trp Gly Thr Glu Ser Thr Thr Val Asn
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 20 25 30

Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val Gly Asn
 35 40 45

Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn Ala Phe
 50 55 60

Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe Leu Cys
 65 70 75 80

Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe Cys Ser
 85 90 95

Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Thr Val Met Thr Cys Ala
 100 105 110

Tyr Leu Ala Gly Leu Ser Met Leu Ser Thr Val Ser Thr Glu Arg Cys

00822T E2E05260

80

$\langle 210 \rangle$	26
$\langle 211 \rangle$	393

Ser Ala Tyr Phe Thr Thr Glu Thr Val Leu Val Ile Val Lys Ser Gln
195 200 205

Glu Lys Ile Phe Cys Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr
210 215 220

Tyr Lys Ser Tyr Phe Leu Phe Ile Phe Gly Ile Glu Phe Val Gly Pro
225 230 235 240

Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp
245 250 255

Phe Lys Ala Val Pro Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu
260 265 270

Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala
275 280 285

Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp
290 295 300

Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe
305 310 315 320

Tyr Ile Val Glu Cys Ile Ala Met Ser Asn Ser Met Ile Asn Thr Leu
325 330 335

Cys Phe Val Thr Val Lys Asn Asp Thr Val Lys Tyr Phe Lys Lys Ile
340 345 350

Met Leu Leu His Trp Lys Ala Ser Tyr Asn Gly Gly Lys Ser Ser Ala
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Asp Leu Asp Leu Lys Thr Ile Gly Met Pro Ala Thr Glu Glu Val Asp
370 375 380

Cys Ile Arg Leu Lys
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<210> 28
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<213> Synthetic Substrate

<400> 28

Ala Pro Arg Thr Pro Gly Gly Arg Arg
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<210> 29
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<210> 30
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<400> 30
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<210> 31
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<220>
 <223> Novel Sequence

<400> 31
 taggcacagg tcatcacag

19

<210> 32
 <211> 18
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<220>
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<400> 32
 ttggacgcca ggaaggtg

18

<210> 33
 <211> 26
 <212> DNA
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<220>
 <223> Novel Sequence

<400> 33
 gcctggagcc tgtcttttct gttctc

26

<210> 34
 <211> 28
 <212> DNA
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<400> 34
 gtagatgagg gggttgatgg cactattc

28

THEORY

19

21

250

235

240

Leu Leu Gln Gly Arg Leu Asp Phe Pro Gly Phe Val Gln Thr Ser Leu
245 250 255

Ala Thr Leu Arg Phe Cys Tyr Ile Val Gly Leu Ser Leu Leu Ala Ala
260 265 270

Val Ser Val Glu Gln Cys Leu Ala Ala Leu Phe Pro Ala Trp Tyr Ser
275 280 285

Cys Arg Arg Pro Arg His Leu Thr Thr Cys Val Cys Ala Leu Thr Trp
290 295 300

Ala Leu Cys Leu Leu Leu His Leu Leu Leu Ser Gly Ala Cys Thr Gln
305 310 315 320

Phe Phe Gly Glu Pro Ser Arg His Leu Cys Arg Thr Leu Trp Leu Val
325 330 335

Ala Ala Val Leu Leu Ala Leu Leu Cys Cys Thr Met Cys Gly Ala Ser
340 345 350

Leu Met Leu Leu Leu Arg Val Glu Arg Gly Pro Gln Arg Pro Pro Pro
355 360 365

Arg Gly Phe Pro Gly Leu Ile Leu Leu Thr Val Leu Leu Phe Leu Phe.
370 375 380

Cys Gly Leu Pro Phe Gly Ile Tyr Trp Leu Ser Arg Asn Leu Leu Trp
385 390 395 400

Tyr Ile Pro His Tyr Phe Tyr His Phe Ser Phe Leu Met Ala Ala Val
405 410 415

His Cys Ala Ala Lys Pro Val Val Tyr Phe Cys Leu Gly Ser Ala Gln
420 425 430

Gly Arg Arg Leu Pro Leu Arg Leu Val Leu Gln Arg Ala Leu Gly Asp
435 440 445

Glu Ala Glu Leu Gly Ala Val Arg Glu Thr Ser Arg Arg Gly Leu Val
450 455 460

Asp Ile Ala Ala Ala Leu Gly Pro Pro Thr Pro Ala Ala Ala Pro Val
465 470 475 480

Arg Gln Glu Gly Asp Val Gly Lys Val Val Gly Ser Glu Ala Gly Ala
485 490 495

Ser Arg Thr Trp Arg Arg Pro Trp Trp Val Thr Arg Ser Cys Ala Val
500 505 510

Lys Val Val Thr Leu Gly Leu Glu His Glu Ala Pro Leu Gly Gly Ser
515 520 525

Trp Lys
530

$\langle 210 \rangle$	43
$\langle 211 \rangle$	1612

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	35.2	12.5	22	65	0.15	3.2	0.98
Gender	1.2	0.4	1	2	0.05	2.8	0.99
Education	12.5	2.1	9	16	0.25	3.5	0.97
Income	1500	500	800	3000	0.35	3.8	0.96
Health	2.5	0.8	1	4	0.10	3.1	0.99
Stress	3.2	1.1	1	5	0.20	3.4	0.98
Workload	4.5	1.5	2	7	0.30	3.7	0.97
Job Satisfaction	3.8	1.2	2	5	0.18	3.3	0.98
Organizational Commitment	4.2	1.3	3	6	0.22	3.6	0.97
Turnover Intent	1.8	0.9	1	4	0.12	3.2	0.99
Work-Life Balance	3.5	1.0	2	5	0.15	3.3	0.98
Employee Engagement	4.0	1.1	3	5	0.18	3.4	0.97
Perceived Stress	3.0	1.0	1	5	0.20	3.5	0.96
Job Involvement	4.3	1.2	3	5	0.15	3.3	0.98
Organizational Identification	4.1	1.1	3	5	0.18	3.4	0.97
Work-Life Balance	3.5	1.0	2	5	0.15	3.3	0.98
Employee Engagement	4.0	1.1	3	5	0.18	3.4	0.97
Perceived Stress	3.0	1.0	1	5	0.20	3.5	0.96
Job Involvement	4.3	1.2	3	5	0.15	3.3	0.98
Organizational Identification	4.1	1.1	3	5	0.18	3.4	0.97

<212> DNA
<213> Homo sapiens

<400> 43
cagtgagccg agatggtgcc attgcactct agcctggggc aacagagcca gactccatct 60
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tctcagaccc tctccccaca tctcctgggc cctgccccca cctggcgtag agggaccagc 180
cccacggaag gctcttgagg ccaggtaacc atggggaggg gaggaatggg gacaccttcc 240
tcttgagtgt cttaggggaag agaagcttag gtcaggtggc tgagggtgga aatgagagag 300
gggtctcctc ctggagggtc tcaccattcc cttggtcacc caccctaact tcatctcccc 360
tgatgtgggg aggagcaggg ggcattgatt cctgagcccc agactcaact gttgtggttt 420
acaggggcat caggagagag agcgagcaga acacactcct gcagcatccc ctggcccccc 480
gccccatgat ggagcccaga gaagctggac agcacgtggg ggccgccaac ggcgcccagg 540
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tgctggggaa tggggcagtc ctctggctgc tcagctccaa tgtctacaga aacccttcg 660
ccatctacct cctggacgtg gcctgcggg atctcatctt ccttggctgc cacatgggtg 720
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ctggggccag ccggacctg aggaggcctt ggtgggtgac ccggtcatgt gctgtcaaag 1560
ttgtgacctc tggctctggag catgaggctc ccctgggagg cagctggaaa gg 1612

<210> 44
<211> 311

09750373.2800

Gly Leu Val Asp Ile Ala Ala
305 310

<210> 45
<211> 939
<212> DNA
<213> Homo sapiens

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gggaatgggg cagtcctctg gctgctcagc tccaatgtct acagaaaccc cttcgccatc 180
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cagtgcctgg ccgccctctt cccagcctgg tactcgtgcc gccgcccacg ccacctgacc 420
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gcctgcaccc agttcttcgg ggagcccagc cgccacttgt gccggacgct gtggctggtg 540
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ctcacgctcc tctcttctc cttctgcggc ctgcccttcg gcactctactg gctgtcccgg 720
aacctgctct ggtacatccc ccactacttc taccattca gcttcctcat ggccgccgtg 780
cactgcgcgg ccaagcccgt cgtctacttc tgccctgggca gtgccaggg ccgcaggctg 840
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gagacctccc gccggggcct ggtggacata gcagcctga 939

<210> 46
<211> 311
<212> PRT
<213> Homo sapiens

<400> 46

Met Met Glu Pro Arg Glu Ala Gly Gln His Val Gly Ala Ala Asn Ser
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Ala Gln Glu Asp Val Ala Phe Asn Leu Ile Ile Leu Ser Leu Thr Glu
20 25 30
Gly Leu Gly Leu Gly Gly Leu Leu Gly Asn Gly Ala Val Leu Trp Leu
35 40 45
Leu Ser Ser Asn Val Tyr Arg Asn Pro Phe Ala Ile Tyr Leu Leu Asp
50 55 60

<210> 48
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Novel Sequence

<400> 48
ctctacacca gactgcttct cgacatctc

29

<210> 49
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Novel Sequence

<400> 49
agatggagac caccatgggg ttcac

25

<210> 50
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Novel Sequence

<400> 50
gggttatattt agtctgatgc agtccacctc

30

<210> 51
<211> 35
<212> DNA
<213> Artificial

<220>
<223> Novel Sequence

<400> 51
gatcgaattc atgatggagc ccagagaagc tggac

35

<210> 52
<211> 34
<212> DNA
<213> Artificial

<220>
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<400> 52
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34

<210> 53

<211> 20
<212> DNA
<213> Artificial

<220>
<223> Novel Sequence

<400> 53
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<210> 54
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<212> DNA
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<220>
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<400> 54
ccgcaggagc aatgaaaatc ag

22

<210> 55
<211> 22
<212> DNA
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<220>
<223> Novel Sequence

<400> 55
ctgagcatgg atccaaccac cc

22

<210> 56
<211> 29
<212> DNA
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<220>
<223> Novel Sequence

<400> 56
ctctacacca gactgcttct cgacatctc

29

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